

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANTS: Chatterjee, Deb K.
Solus, Joseph
Yang, Shuwei

(ii) TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof

(iii) NUMBER OF SEQUENCES: 93

10 (iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)
(B) FILING DATE: 06-FEB-1998
(C) CLASSIFICATION:

25 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)
(B) FILING DATE: 06-JAN-1998
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/037,393
(B) FILING DATE: 07-FEB-1997
(C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0942.4250002

40 (ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2682 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 5 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGAGAC	TATTTCTCTT	TGATGGCACA	GCCCTGGCCT	ACAGGGCATA	TTACGCCCTC	60
GACAGATCCC	TTTCCACATC	CACAGGAATT	CCAACGAACG	CCGTCTATGG	CGTTGCCAGG	120
10 ATGCTCGTTA	AATTCAATTAA	GGAACACATT	ATACCCGAAA	AGGACTACGC	GGCTGTGGCC	180
TTCGACAAGA	AGGCAGCGAC	GTTCAAGACAC	AAACTGCTCG	TAAGCGACAA	GGCGCAAAGG	240
CCAAAGACTC	CGGCTCTTCT	AGTTCAAGCAG	CTACCTTACA	TCAAGCGGCT	GATAGAAGCT	300
CTTGGTTTCA	AAGTGCTGGA	GCTGGAGGGA	TACGAAGCAG	ACGATATCAT	CGCCACGCTT	360
GCAGTCAGGG	CTGCACGTTT	TTTGATGAGA	TTTCATTAA	TAACCGGTGA	CAAGGATATG	420
15 CTTCAACTTG	TAAACGAGAA	GATAAAGGTC	TGGAGAAATCG	TCAAGGGGAT	ATCGGATCTT	480
GAGCTTTACG	ATTCGAAAAAA	GGTGAAAGAA	AGATAACGGTG	TGGAACCACA	TCAGATAACCG	540
GATCTTCTAG	CACTGACGGG	AGACGACATA	GACAACATTG	CCGGTGTAAAC	GGGAATAGGT	600
GAAAAGACCG	CTGTACAGCT	TCTCGGCAAG	TATAGAAATC	TTGAATACAT	TCTGGAGCAT	660
GCCC GTGAAC	TCCCCCAGAG	AGTGAGAAAG	GCTCTCTTGA	GAGACAGGGGA	AGTTGCCATC	720
20 CTCAGTAAAA	AACTTGCAAC	TCTGGTGACG	AACGCACCTG	TTGAAGTGGG	CTGGGAAGAG	780
ATGAAATACA	GAGGATACGA	CAAGAGAAAA	CTACTTCCGA	TATTGAAAGA	ACTGGAGTTT	840
GCTTCCATCA	TGAAGGAACT	TCAACTGTAC	GAAGAACGAG	AACCCACCGG	ATACGAAATC	900
GTGAAGGATC	ATAAGACCTT	CGAAGATCTC	ATCGAAAAGC	TGAAGGAGGT	TCCATCTTT	960
GCCC GTGACC	TTGAAACGTC	CTCCCTTGAC	CCGTTCAACT	GTGAGATAGT	CGGCATCTCC	1020
25 GTGTCGTTCA	AACCGAAAAC	AGCTTATTAC	ATTCCACTTC	ATCACAGAAA	CGCCCAGAAT	1080
CTTGATGAAA	CACTGGTGCT	GTCGAAGTTG	AAAGAGATCC	TCGAAGACCC	GTCTTCGAAG	1140
ATTGTGGGTC	AGAACCTGAA	GTACGACTAC	AAGGTTCTTA	TGGTAAAGGG	TATATCGCCA	1200
GTTTATCCGC	ATTTGACAC	GATGATAGCT	GCATATTGTC	TGGAGCCAAA	CGAGAAAAAA	1260
TTCAATCTCG	AAGATCTGTC	TTTGAAATT	CTCGGATACA	AAATGACGTC	TTATCAGGAA	1320

CTGATGTCGT	TTTCCTCACC	ACTTTTGTT	TTCAGCTTG	CGGATGTTCC	GGTAGACAAG	1380	
GCTGCGAACT	ACTCCTGCGA	GGATGCAGAC	ATCACTTATA	GGCTCTACAA	GATACTCAGC	1440	
ATGAAGCTCC	ATGAAGCGGA	ACTTGAGAAC	GTCTTCTACA	GGATAGAGAT	GCCGTTGGTG	1500	
AACGTTCTTG	CACGCATGGA	ATTGAACGGG	GTGTATGTGG	ACACAGAATT	CCTGAAAAAG	1560	
5	CTCTCGGAGG	AGTACGGCAA	AAAGCTCGAG	GAACCTGGCCG	AAAAAAATCTA	CCAGATAGCA	1620
GGTGAGCCCT	TCAACATCAA	TTCTCCAAAA	CAGGTTTCAA	AGATCCTTTT	TGAGAAGCTG	1680	
GGAATAAAAC	CCCGTGGAAA	AACGACAAAA	ACAGGAGAGT	ACTCTACCAG	GATAGAGGTG	1740	
TTGGAAGAGA	TAGCGAATGA	GCACGAGATA	GTACCCCTCA	TTCTCGAGTA	CAGAAAGATC	1800	
CAGAAACTGA	AATCGACCTA	CATAGACACC	CTTCCGAAAC	TTGTGAACCC	GAAAACCGGA	1860	
10	AGAATTCATG	CATCTTCCA	CCAGACGGGT	ACCGCCACTG	GCAGGTTGAG	TAGCAGTGAT	1920
CCAAATCTTC	AGAATCTTCC	GACAAAGAGC	GAAGAGGGAA	AAGAAATTAG	AAAAGCGATT	1980	
GTGCCCCAGG	ATCCAGACTG	GTGGATCGTC	AGTGCAGGATT	ATTCCCAAAT	AGAACTCAGA	2040	
ATCCTCGCTC	ATCTCAGTGG	TGATGAGAAC	CTTGTGAAGG	CCTTCGAGGA	GGGCATCGAT	2100	
GTGCACACCT	TGACTGCCCTC	CAGGATCTAC	AACGTAAAGC	CAGAAGAAGT	GAACGAAGAA	2160	
15	ATGCGACGGG	TTGGAAAGAT	GGTGAACCTTC	TCTATAATAT	ACGGTGTAC	ACCGTACGGT	2220
CTTCTGTGA	GACTTGAAT	ACCGGTTAAA	GAAGCAGAAA	AGATGATTAT	CAGCTATTTC	2280	
ACACTGTATC	CAAAGGTGCG	AAGCTACATC	CAGCAGGTTG	TTGCAGAGGC	AAAAGAGAAG	2340	
GGCTACGTCA	GGACTCTCTT	TGGAAGAAAA	AGAGATATTC	CCCAGCTCAT	GGCAAGGGAC	2400	
AAGAACACCC	AGTCCGAAGG	CGAAAAGAATC	GCAATAAACAA	CCCCCATTCA	GGGAACGGCG	2460	
20	GCAGATATAA	TAAAATGGC	TATGATAGAT	ATAGACGAGG	AGCTGAGAAA	AAGAAACATG	2520
AAATCCAGAA	TGATCATTCA	GGTCATGAC	GAACGGTCT	TCGAGGTTCC	CGATGAGGAA	2580	
AAAGAAGAAC	TAGTTGATCT	GGTGAAGAAC	AAAATGACAA	ATGTGGTGAA	ACTCTCTGTG	2640	
CCTCTTGAGG	TTGACATAAG	CATCGGAAAAA	AGCTGGTCTT	GA		2682	

(2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

5 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

10 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

15 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

20 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

25 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

30 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255

DRAFT

	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu			
	260	265	270	
	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln			
	275	280	285	
5	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His			
	290	295	300	
	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe			
	305	310	315	320
10	Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile			
	325	330	335	
	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro			
	340	345	350	
	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser			
	355	360	365	
15	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln			
	370	375	380	
	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro			
	385	390	395	400
20	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro			
	405	410	415	
	Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly			
	420	425	430	
	Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu			
	435	440	445	
25	Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr			
	450	455	460	
	Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser			
	465	470	475	480
30	Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu			
	485	490	495	
	Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr			
	500	505	510	
	Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys			
	515	520	525	
35	Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe			
	530	535	540	
	Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu			

100

545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
565 570 575

5 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
595 600 605

Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
610 615 620

10 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
645 650 655

15 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
675 680 685

Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
690 695 700

20 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
725 730 735

25 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
755 760 765

Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
770 775 780

30 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

35 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880

5 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 677 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 Met Ser Leu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu
 1 5 10 15

Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu
 20 25 30

20 Val Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg
 35 40 45

Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe
 50 55 60

Ala Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr
 65 70 75 80

25 Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu
 85 90 95

Lys Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser
 100 105 110

30 Leu Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys
 115 120 125

Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn
 130 135 140

Leu Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp
 145 150 155 160

Pro Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val
 165 170 175
 Leu Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met
 180 185 190
 5 Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu
 195 200 205
 Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu
 210 215 220
 Leu Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val
 10 225 230 235 240
 Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr
 245 250 255
 Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu
 260 265 270
 15 Glu Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala
 275 280 285
 Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys
 290 295 300
 Leu Ser Glu Glu Tyr Gly Lys Leu Glu Glu Leu Ala Glu Lys Ile
 20 305 310 315 320
 Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val
 325 330 335
 Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr
 340 345 350
 25 Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile
 355 360 365
 Ala Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile
 370 375 380
 30 Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn
 385 390 395 400
 Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala
 405 410 415
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr
 420 425 430
 35 Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp
 435 440 445
 Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg

	450	455	460	
	Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu			
	465	470	475	480
5	Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val			
	485	490	495	
	Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val			
	500	505	510	
	Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg			
	515	520	525	
10	Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe			
	530	535	540	
	Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu			
	545	550	555	560
15	Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp			
	565	570	575	
	Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu			
	580	585	590	
	Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile			
	595	600	605	
20	Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met			
	610	615	620	
	Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val			
	625	630	635	640
25	Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met			
	645	650	655	
	Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile			
	660	665	670	
	Gly Lys Ser Trp Ser			
	675			

30 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu
 1 5 10 15

5 Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys
 20 25 30

Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro
 35 40 45

Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr
 50 55 60

10 Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu
 65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser
 85 90 95

15 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val
 100 105 110

Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala
 115 120 125

Tyr Leu Leu Glu Pro Asn Glu Lys Phe Asn Leu Glu Asp Leu Ser
 130 135 140

20 Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser
 145 150 155 160

Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp
 165 170 175

25 Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu
 180 185 190

Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val
 195 200 205

Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu
 210 215 220

30 Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu
 225 230 235 240

Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile
 245 250 255

35 Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile
 260 265 270

Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr

	275	280	285
	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu		
	290	295	300
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu		
5	305	310	315
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr		
	325	330	335
	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg		
	340	345	350
10	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu		
	355	360	365
	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp		
	370	375	380
15	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala		
	385	390	395
	His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile		
	405	410	415
	Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu		
	420	425	430
20	Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser		
	435	440	445
	Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile		
	450	455	460
25	Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr		
	465	470	475
	Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu		
	485	490	495
30	Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln		
	500	505	510
	Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala		
	515	520	525
	Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala		
	530	535	540
35	Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg		
	545	550	555
	Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu		

565

570

575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val
 580 585 590

5 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser
 595 600 605

Trp Ser
 610

(2) INFORMATION FOR SEQ ID NO:5:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu
 1 5 10 15

Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile
 20 25 30

20 Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu
 35 40 45

Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val
 50 55 60

25 Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly
 65 70 75 80

Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala
 85 90 95

Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly
 100 105 110

30 Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys
 115 120 125

Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu
 130 135 140

Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro

	145	150	155	160
	Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu			
	165	170	175	
5	Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro			
	180	185	190	
	Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu			
	195	200	205	
	Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile			
	210	215	220	
10	Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp			
	225	230	235	240
	Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu			
	245	250	255	
15	Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro			
	260	265	270	
	Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr			
	275	280	285	
	Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu			
	290	295	300	
20	Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg			
	305	310	315	320
	Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu			
	325	330	335	
25	Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr			
	340	345	350	
	Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser			
	355	360	365	
	Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr			
	370	375	380	
30	Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala			
	385	390	395	400
	Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln			
	405	410	415	
35	Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro			
	420	425	430	
	Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr			

	435	440	445
	Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys		
	450	455	460
5	Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro		
	465	470	475
	Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile		
	485	490	495
	Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu		
	500	505	510
10	Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys		
	515	520	525
	Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn		
	530	535	540
15	Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu		
	545	550	555
	Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr		
	565	570	575
	Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala		
	580	585	590
20	Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile		
	595	600	605
	Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg		
	610	615	620
25	Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys		
	625	630	635
	Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys		
	645	650	655
	Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro		
	660	665	670
30	Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr		
	675	680	685
	Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly		
	690	695	700
35	Lys Ser Trp Ser		
	705		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

10 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

15 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

20 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

25 Met Arg Phe Ser Leu Ile Thr Gly Ala Lys Asp Met Leu Gln Leu Val
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

30 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

35 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255

5 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285

10 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320

Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335

15 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365

20 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415

25 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445

30 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480

Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495

35 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510

	Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys			
	515	520	525	
	Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe			
	530	535	540	
5	Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu			
	545	550	555	560
	Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr			
	565	570	575	
10	Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro			
	580	585	590	
	Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile			
	595	600	605	
	Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala			
	610	615	620	
15	Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp			
	625	630	635	640
	Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile			
	645	650	655	
20	Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala			
	660	665	670	
	Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp			
	675	680	685	
	Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu			
	690	695	700	
25	Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu			
	705	710	715	720
	Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val			
	725	730	735	
30	Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala			
	740	745	750	
	Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser			
	755	760	765	
	Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg			
	770	775	780	
35	Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp			
	785	790	795	800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 805 810 815
 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 820 825 830
 5 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 835 840 845
 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Leu
 850 855 860
 10 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880
 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Leu Phe Leu Phe Ala Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15
 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30
 25 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45
 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60
 30 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80
 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95
 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110
 35 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu

	115	120	125
	Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp	Met Leu Gln Leu Val	
	130	135	140
5	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu		
	145	150	155
	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro		
	165	170	175
	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn		
	180	185	190
10	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu		
	195	200	205
	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu		
	210	215	220
15	Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile		
	225	230	235
	Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val		
	245	250	255
	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu		
	260	265	270
20	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln		
	275	280	285
	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His		
	290	295	300
25	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe		
	305	310	315
	Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile		
	325	330	335
	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro		
	340	345	350
30	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser		
	355	360	365
	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln		
	370	375	380
35	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro		
	385	390	395
	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro		
	405	410	415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445

5 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480

10 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525

15 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560

20 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
 595 600 605

25 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
 610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640

30 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685

35 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735

5 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765

10 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
 785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 805 810 815

15 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 835 840 845

20 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Leu
 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

5 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

10 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

15 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

20 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

Ile Pro Asp Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

25 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240

30 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285

35 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320

Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335

5 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365

10 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415

15 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445

20 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480

Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495

25 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525

30 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 565 570 575

35 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
 595 600 605

Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
 610 615 620

5 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655

10 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685

Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700

15 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735

20 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765

Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780

25 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
 785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 805 810 815

30 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
 850 855 860

35 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

15 Asn Ala Val Tyr Asp Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

20 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

25 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
 130 135 140

30 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

35 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240

5 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270

10 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285

Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320

15 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350

20 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400

25 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430

30 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480

35 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525

5 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560

Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 10 565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
 595 600 605

15 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
 610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640

20 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685

25 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720

30 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735

Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765

35 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
 785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 805 810 815

5 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 835 840 845

10 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Leu
 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

15 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu
 1 5 10 15

Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys
 20 25 30

30 Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro
 35 40 45

Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr
 50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu
 65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser
 85 90 95

35 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val

	100	105	110
	Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala		
	115	120	125
5	Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser		
	130	135	140
	Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser		
	145	150	155
	Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp		
	165	170	175
10	Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu		
	180	185	190
	Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val		
	195	200	205
15	Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu		
	210	215	220
	Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu		
	225	230	235
	Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile		
	245	250	255
20	Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile		
	260	265	270
	Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr		
	275	280	285
25	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu		
	290	295	300
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu		
	305	310	315
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr		
	325	330	335
30	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg		
	340	345	350
	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu		
	355	360	365
35	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp		
	370	375	380
	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala		
	385	390	395

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile
 405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu
 420 425 430

5 Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser
 435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile
 450 455 460

10 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr
 465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu
 485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln
 500 505 510

15 Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala
 515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala
 530 535 540

20 Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg
 545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu
 565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val
 580 585 590

25 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser
 595 600 605

Trp Ser
 610

(2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /note= "'Xaa' is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Pro Val Ala Phe Asp Ser Glu Thr Ser Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ile Val Ser Asp Ile Glu Ala Asn Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACGTTTCAA GCGCTAGGGC AAAAGA

26

(2) INFORMATION FOR SEQ ID NO:23:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTATATTATA GAGTAGTTAA CCATCTTCC A

31

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10 Phe Leu Phe Asp Gly Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

20 Leu Leu Val Asp Gly His
 1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

30 Ser Leu Ile Thr Gly Asp Lys Asp Met Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10 Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAGGCCAGG GCTGTGCCGG CAAAGAGAAA TAGTC

35

20 (2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGCATATC CTTGGCGCCG GTTATTATGA AAATC

35

(2) INFORMATION FOR SEQ ID NO:30:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCAAGACGG GTACCGCCAC TGGCAGGTTG

30

(2) INFORMATION FOR SEQ ID NO:31:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:32:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25 TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:33:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTTCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:34:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TATAGAGTAG TTAACCATCT TTCCAACCCG ATGCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:35:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGATGGTTA ACGCGTCTAT AATATAACGG

29

(2) INFORMATION FOR SEQ ID NO:36:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAGAGGCAC AGAGAGTTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATTATA GAGGAGTTAA CCATCTTCC

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 AAGATGGTTA ACTTCTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

48

(2) INFORMATION FOR SEQ ID NO:40:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATAGAGTAG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC

48

10 (2) INFORMATION FOR SEQ ID NO:41:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTGGCCGCC CGATGCATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:42:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGCCGCC CGCTTCATGA GGGGGTCCAC

30

(2) INFORMATION FOR SEQ ID NO:43:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGCCGCC CTGTACATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 GTATATTATA GAGGTGTTAA CCATCTTCC

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGAGACCGG AATTCTCCTT CATTAATTCC TATA

34

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGAGACCCT GGAACATATAG GAATTAATGA AGGAGAATTC CGGTCTCCC

49

(2) INFORMATION FOR SEQ ID NO:47:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTATTTGGT ATGCTTGTGC

20

(2) INFORMATION FOR SEQ ID NO:48:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTATTTGGA ATATATGTGC CT

22

(2) INFORMATION FOR SEQ ID NO:49:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACGAACATTC TACAAGTTAC

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTCAGAGAA ACTGACCTGT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

20 GATAAATGCC AAACATGTTG T

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCTCTCAGG ATTCCTCCA

20

(2) INFORMATION FOR SEQ ID NO:53:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTGAGAC CTCTGTGTCC

20

10 (2) INFORMATION FOR SEQ ID NO:54:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTCAGAAGA AACAGTGATG GT

22

(2) INFORMATION FOR SEQ ID NO:55:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGGAGTCGC AAGCTGAAGT AGC

23

(2) INFORMATION FOR SEQ ID NO:56:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCCTGAGTGA CAGAGTGAGA ACC

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

15 CCCACTAGGT TGTAAGCTCC ATGA

24

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TACTATGTGC CAGGCTCTGT CCTA

24

25 (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTCATGAAG GTGACAGTTC

20

(2) INFORMATION FOR SEQ ID NO:60:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGTTGTTGA CCTATTGCAT

20

(2) INFORMATION FOR SEQ ID NO:61:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCTCTGTTCT CCTCCCTGTT

20

(2) INFORMATION FOR SEQ ID NO:62:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTATTGGCC TTGAAGGTAG

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCCCCTGTT GGAACCATGA CTG

23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

20 TACATAGCGA GACTCCATCT CCC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTATGCGAG CGTATGGATA

20

(2) INFORMATION FOR SEQ ID NO:66:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CACCACCATT GATCTGGAAG

20

10 (2) INFORMATION FOR SEQ ID NO:67:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCAACCACAC TGGGAA

16

(2) INFORMATION FOR SEQ ID NO:68:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACAGTTGCC CACGGT

16

(2) INFORMATION FOR SEQ ID NO:69:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATGAAATGC TGACTGGGTA

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

15 TCAATTATG TGCAGCCAAT

20

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATAGCGAGA CTCCATCTCC

20

25 (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGAGAGGGC AAAGATCGAT

20

(2) INFORMATION FOR SEQ ID NO:73:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AACACTAGTG ACATTATTT CA

22

(2) INFORMATION FOR SEQ ID NO:74:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGCTAGGCCT GAAGGCTTCT

20

(2) INFORMATION FOR SEQ ID NO:75:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCCTAGTGGA TGATAAGAAT AATC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGACAGATGA TAAATACATA GGATGGATGG

30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

20 TTCTCTTACA ACAC TGCCCC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATTTGGATGG CTTGACAGAG

20

(2) INFORMATION FOR SEQ ID NO:79:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACATTCTAAG ACTTTCCCAA T

21

10 (2) INFORMATION FOR SEQ ID NO:80:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGAGCATGCA CCCTGAATTG

20

(2) INFORMATION FOR SEQ ID NO:81:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGAACCATG CGATACGACT

20

(2) INFORMATION FOR SEQ ID NO:82:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CATTCCTAGA TGGGTAAAGC

20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

15 GCTTAGTCAT ACGAGCGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCACAGCCA TGTAAACC

18

25 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CCCCGGAGCA AGTTCA

16

(2) INFORMATION FOR SEQ ID NO:86:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGCCCAAAG CCAGATTA

18

(2) INFORMATION FOR SEQ ID NO:87:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATATGTGAGT CAATTCCCCA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTATTAGTC AATGTTCTCC AG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAGCTGCCCT AGTCAGCAC

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20 GCTTCCGAGT GCAGGTCACA

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATTCTGGCG CACAAGAGTG A

21

(2) INFORMATION FOR SEQ ID NO:92:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACATCTCCCC TACCGCTATA

20

10 (2) INFORMATION FOR SEQ ID NO:93:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAAGTTCACCA ATCCGGCCGA CCCGTCGCAT TTC

33